Recent variations in Arctic and Antarctic sea-ice covers

Gloersen, Per; Campbell, William J.

Abstract

Variations in the extents of sea-ice cover at the poles and the areas of open water enclosed within them were observed every other day during the interval 1978-1987 by a satellite-borne scanning multispectral microwave radiometer. A band-limited regression technique shows that the trends in coverage of the Arctic and Antarctic sea-ice packs are not the same. During these nine years, there are significant decreases in ice extent and open-water areas within the ice cover in the Arctic, whereas in the Antarctic, there are no significant trends.

the number of observations. W was chosen so that $W = 4/N$. The bandpass filter used in this approach consists of the first eight eigenvectors and the corresponding eigenvalues of the matrix, U, obtained from its singular value decomposition[11], designated as an $8 \times 1,612$ matrix, V, and an 8×8 diagonal matrix, S, respectively. Because of the rapid falloff of the magnitudes of the eigenvalues, a very close approximation (called elsewhere truncated series regression[5]) to the original matrix, U, is obtained as follows:

$$U = VSV' \qquad (2)$$

where the prime indicates a matrix transpose. The method continues by formulating the offset and trend in a $1,612 \times 2$ design matrix, D, and obtaining the offset and trend in a coefficient vector, $\mathbf{a}$, as follows:

$$\mathbf{a} = (D'UD)^{-1}(D'U\mathbf{y}) \qquad (3)$$

where $\mathbf{y}$ is the data vector. The standard deviations of $\mathbf{a}$ are also obtained from D, V, and $\mathbf{y}$, in a manner[5] too lengthy to be outlined here.

When this method is applied to the data on the extent of Arctic sea ice obtained from SMMR, a trend of -0.0315×10^6 km^2 per year is found, with a standard deviation of 0.0143×10^6 km^2 per year. Over the SMMR operational period of 8.8 years, this represents a $2.1 \pm 0.9\%$ decline in the Arctic sea-ice extent. As the basis function of eight eigenvalues was used to determine an offset and trend, the net number of degrees of freedom to be used in the statistical, single-sided t-test[5] is six, and the confidence level of the determination is 96.5%, based on the ratio of the trend to the standard deviation, which is 2.20. The trend so determined is smaller than the -4% and -5% trends reported earlier[4] for the maximum and minima, respectively, of the Arctic sea-ice extent, but as mentioned above, these earlier calculations were based on a standard linear regression analysis of uncorrected SMMR data of annual extrema and a lower (8–12%) ice concentration for the ice edge than the 15% used here. The Arctic decline reported here is greater than the -1.4% reported recently[12] for an eight-year interval of annually averaged uncorrected SMMR data. On the other hand, we have found that annually averaging the corrected data over an interval of eight years (so as to average over complete seasonal cycles) before running a linear regression, as done with the uncorrected data earlier[12], gives a trend of -2.2% for the Arctic extent, but the statistical significance of the trend so determined is not valid.

Application of the BLR technique to Arctic open-water area within the ice cover yields a trend of $-3.5 \pm 2.0\%$, at a confidence level of 93.5%. Thus the trends for both the Arctic ice extent and the open water are negative. These trends indicate that for the Arctic the area covered by sea ice decreased less than its ice extent. Application of the technique to the Antarctic sea-ice extent and open-water area leads to statistically insignificant results, as the standard deviations of the trends are greater than the trends themselves. The results are summarized in Table 1 and illustrated in Figs 1 and 2.

We are confident that the BLR analysis reported here more accurately represents the actual trends than results based on ordinary linear regression analysis of uncorrected SMMR data, whether on the annual averages or annual extrema.

Discussion

A number of studies have indicated that changes in the global average air temperature might be detectable by observing changes in the extents of the polar sea-ice covers[8,9,13–17,23]. The Nimbus-7 SMMR observations give us a unique look at the variations of these extents every two days for almost a decade, and thus provide the most accurate and comprehensive such record yet obtained. The trend obtained by BLR analysis of the Arctic sea-ice extent (Table 1) may be a signal of climate change. It should be said that the near-decade of SMMR observations is not sufficiently long to establish a climate trend clearly. What

sea-ice data are available to extend the record? The interval 1973–76 was covered by an earlier passive microwave radiometer flown in space, the electrically scanned microwave radiometer (ESMR) on board the Nimbus-5 satellite. We have not attempted to treat the ESMR data in the same manner as the SMMR data, because they are not as accurate. The sea-ice record for the time before ESMR is made up largely of data from visible-light sensors flown on the early meteorological satellites; the combination of polar clouds and poor lighting conditions has resulted in a fragmented data set of limited quality for the sea-ice extent.

Whether or not the SMMR record of the decrease in the extents of the Arctic sea-ice cap signals a climate change is therefore an open question. These findings are, however, consistent with records of significant changes in other large-scale phenomena which have occurred over longer periods, including the SMMR decade. A marked increase in the global atmospheric air temperature[18,19] commenced in 1974 and persisted until the 1980s, which became distinctly the warmest interval in the record lasting for more than 100 years, albeit in the lower latitudes. A warming of the Alaskan Arctic permafrost, typically 2–4 °C, commenced during the past 100 years, and during the SMMR lifetime the average increase[20] was 0.5 °C. A decrease in the extent of the Arctic sea-ice cover has been cited as a possible cause for this warming[20], but any permafrost warming corresponding to a change in sea-ice extent would have occurred over much longer times than addressed here. On the other hand, there has been no evidence of warming in ocean surface temperatures in the northern hemisphere during this interval[21].

We do not know the causes of this asymmetry between the hemispheres, with a significant decrease in Arctic sea-ice extent,
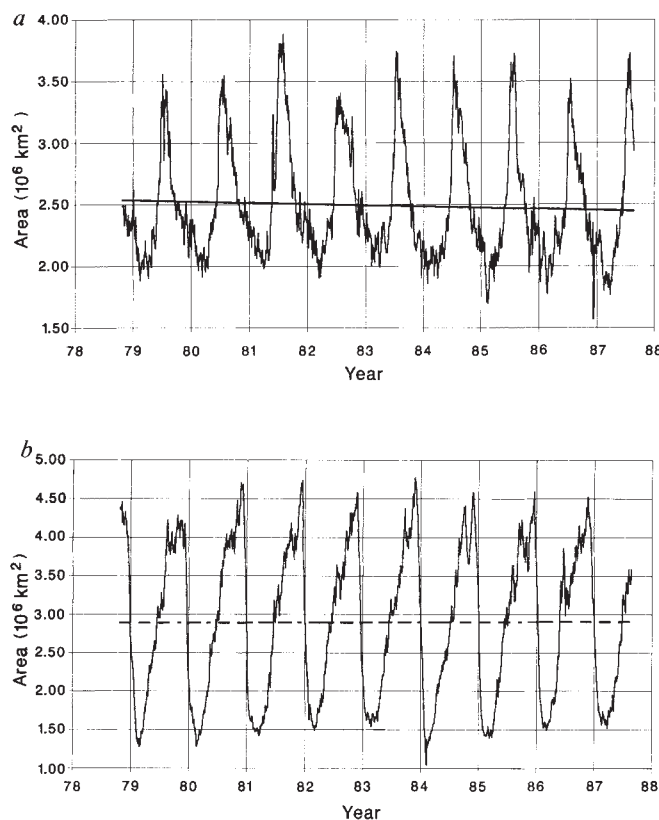
FIG. 2 Open water within the ocean–ice boundary (leads and polynyas) for a, the Arctic and b, the Antarctic from 25 October 1978 to 20 August 1987, and their trends. The Arctic trend (solid line) is a 3.5% decline over the 8.8-year interval under discussion, and is significant to the 93% confidence level. The Antarctic trend (dashed line) is statistically insignificant.

but no corresponding decrease in the Antarctic. It is interesting to note that a recent simulation with a coupled ocean–atmosphere model[22] of the atmospheric response to a doubling of the global CO_2 level over a century shows an interhemispheric asymmetry in the warming of surface air temperatures, with the Antarctic increasing very slowly and the Arctic faster.

We do know that sea ice exists in those parts of the Earth where global warming is expected to be the greatest. We also know that the sea-ice covers, with their high albedos and insulating effect between the polar atmospheres and oceans, are a key part of the climate machine. That the variations of the Arctic and Antarctic sea-ice extents and enclosed open water have behaved asymmetrically over nearly a decade is a new finding which must be considered in predictions of global change. □

1. Badgley, F. I. in *Proc. Symp. Arctic Heat Budget and Atmospheric Circulation* (ed. Fletcher, J. O.) 267–277 (1966).
2. Campbell, W. J. et al. *J. geophys. Res.* **92,** 6805–6824 (1987).
3. Cavalieri, D. J., Gloersen, P. & Campbell, W. J. *J. geophys. Res.* **89,** 5355–5369 (1984)
4. Gloersen, P. & Campbell, W. J. *J. geophys. Res.* **93,** 10666–10674 (1988).
5. Lindberg, C. R. *J. R. stat. Soc.* B (submitted).
6. Francis, E. A., thesis, Univ. of Oregon State (1987).
7. Gloersen, P. & Cavalieri, D. J. *J. geophys. Res.* **91,** 3913–3919 (1986).
8. Zwally, H. J. et al. *NASA SP*-459 (U.S. GPO, Washington DC, 1983).
9. Parkinson, C. L. et al. *NASA SP*-489 (U.S. GPO, Washington DC, 1987).
10. Kuo, C., Lindberg, C. & Thomson, D. J. *Nature* **343,** 709–714, (1990).
11. Press, W. H., Flannery, B. P., Teukolsky, S. A. & Vetterling, W. T. *Numerical Recipes in C* (Cambridge University Press, 1989).
12. Parkinson, C. L. & Cavalieri, D. J. *J. geophys. Res.* **94,** 14499–14523 (1989).
13. Sissla, J. F., Sabatini, R. R. & Ackerman, H. J. *Polar Res.* **16,** 367–373 (1972).
14. Streten, N. A. *Arch. Meteorol. geophys. Bioklimatol. Ser.* A**22,** 129–134 (1973).
15. Budd, W. F. *J. Glaciol.* **15,** 417–426 (1975).
16. Kukla, G. & Gavin, J. *Science* **215,** 497–503 (1981).
17. Carsey, F. D. *J. geophys. Res.* **87,** 5809–5835 (1982).
18. Jones, P. D. et al. *Nature* **322,** 790 (1988).
19. Hansen, J. & Lebedeff, S. *Geophys. Res. Lett.* **15,** 323–326 (1988).
20. Lachenbruck, A. H., Cladouhos, T. T. & Saltus, R. W. *Permafrost* **3,** 9–17 (ed. Senneset, K.) (Tapir, Trondheim, Norway, 1988).
21. Reynolds, W. R., Folland, C. K. & Parker, D. E. *Nature* **341,** 728–731 (1989).
22. Stouffer, R. J., Manabe, S. & Bryan, K. *Nature* **342,** 660–662 (1989).
23. Zwally, H. J., Parkinson, C. L. & Comiso, J. C. *Science* **220,** 1005–1012 (1983).

Chaperonin-mediated protein folding at the surface of groEL through a 'molten globule'-like intermediate

Jörg Martin, Thomas Langer, Raina Boteva*, Andrea Schramel*, Arthur L. Horwich† & F.-Ulrich Hartl‡

Institut für Physiologische Chemie der Universität München, Goethestrasse 33, W-8000 München 2, Germany
* Zoologisches Institut der Universität München, Luisenstrasse 14, W-8000 München 2, Germany
† Howard Hughes Medical Institute and Department of Human Genetics, Yale School of Medicine, 333 Cedar Street, New Haven, Connecticut 06510, USA

Folding of two monomeric enzymes mediated by groE has been reconstituted *in vitro*. The groEL protein stabilizes the polypeptides in a conformation resembling the 'molten globule' state. Mg–ATP and groES then promote the acquisition of ordered tertiary structure at the surface of groEL. Folding requires the hydrolysis of about 100 ATP molecules per protein monomer. This active process of surface-mediated chain folding might represent a general mechanism for the formation of protein structure *in vivo*.

LITTLE is known about the mechanisms by which newly synthesized proteins fold inside cells. For many proteins, folding *in vivo* may not be a spontaneous process. Several components are involved in mediating protein folding in a variety of cell types and compartments[1-3]. With the exception of protein disulphide isomerase and peptidyl prolyl isomerase, they have been classified as 'molecular chaperones'[3,4] or 'polypeptide chain binding proteins'[5] on the basis of their ability to prevent the formation of wrong aggregates by binding to unfolded or partially denatured proteins. The heat-shock proteins of the hsp70

and hsp60 families are typical representatives of this group of components[5-7].

The essential function in protein folding of the members of the hsp60 family has been demonstrated *in vivo* and *in vitro*. These so-called 'chaperonins'[8] comprise the groEL protein of *Escherichia coli* and other bacteria[8-17], the rubisco-binding protein of chloroplasts[18-20] and the mitochondrial hsp60[21-25]. They form complexes with ATPase activity composed of 14 subunits with a relative molecular mass of 60,000 (M_r 60K) which are arranged in two stacked seven-subunit rings. The groEL protein and the mitochondrial hsp60 functionally cooperate with groES[26,27], a ring-shaped complex of seven roughly 10K subunits, which inhibits the ATPase activity of groEL[26,28]. The groE proteins are required for λ-phage head assembly[9,10]. The ribulose 1,5-bisphosphate carboxylase oxygenase (Rubisco) binding-protein mediates the assembly of hexadecameric Rubisco in chloroplasts[18-20]. The groE-dependent assembly of dimeric prokaryotic Rubisco has been reconstituted *in vitro*[13,28]. The mitochondrial hsp60 is necessary not only for the oligomeric assembly of proteins[23,25] but also for the chain folding of monomeric polypeptides[24]. The molecular mechanism of this ATP-driven process remains unknown.

Using the groEL and groES proteins of *E. coli*, we have reproduced the chaperonin-dependent folding of two monomeric enzymes, dihydrofolate reductase (DHFR) and rhodanese. Folding reactions were monitored by measuring intrinsic tryptophan fluorescence, adsorption of the fluorescent dye anilino-napththalene-sulphonate, protease sensitivity and enzyme activity. We find that groEL stabilizes an early intermediate on the folding pathway seemingly equivalent to the folding

‡ To whom correspondence should be addressed. Address after November 1: Laboratory of Cellular Biochemistry, Rockefeller Research Laboratory, Sloan-Kettering Institute, New York, New York 10021, USA.